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Minimum
Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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        205
181
168
161
161
152
152
152
149
                                                                                                                                                                                                                                                                           No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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length: 2000000000
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20:
21:
23:
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Gapop 10.0 ,
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3945
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(cgn1_7/ptodata/1/---
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/ptodata/1/paa/US092_COMB.pep:*
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/ptodata/1/paa/US095_COMB.pep:*
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                   US-09-134-000-6122

US-09-107-532-4518

US-09-134-000-4971

US-09-071-035-402

US-09-071-035-402

US-08-851-567B-49

US-08-851-567B-47

US-09-337-536-2

US-09-200-650-5
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Sequence 6122, Ap
Sequence 4518, Ap
Sequence 404, App
Sequence 402, App
Sequence 402, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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-60-173-464-	-60-167-2	-09-251-645-	-09-252-691C	-09-252	-09-084-517-	8-957	-08-915	-08-70	-	422-711-	-496-1	-US97-15	4	-09-071	-09-071	8-993-002A-61	-09-450	-09-386	US-09-386-962B-10	9	PCT-US99-19728-10	US-08-373-957-2	48	827-356-3	-09-147-405-	-447-031-	-07-861-804-	-60-191-681-167	-60-191-	0-269-308-443	-09-134-000-661	9-071-035-4	-09-071-035-46	US-09-071-035-458
1551,	188		101	1010		10,	10,	e 10,	10, ;	10,	10,	10, Apr	6043,	418,	420, 2	6136,	5309, A	10, App	10,	e 10,	10	2, Appl	4893,	3416	e 15	'n	2, Appl	1674,	2094,	4438,	6612;	466,	462,	Sequence 458, App

ALIGNMENTS

US-09-134-000-6122

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Sequence 6122, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: MCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS;
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 6122
LENGTH: 1154
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
701 RKQVTDTANWQTGYIKLSKPENDTSNSWERKNVTQLSKTADESYQEVLGLPQYNNQGQAF 760
                                                                                                                                                                                                   602 VSLTGATINSNEIY------LGKGQEIQIHYQVR--IQTESENFKPDFWYQMNGRTT 650
                                                                                                                                                                                                                                             96 VNLEGS--RSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFED-----YAMSPRIT 147
                                              ESNLVSTS-----QLSLMRQALKQLIDPNLATKMPKQVPDDFQ--LSIFESEDKGDKY 258
                                                                                                FQPLATAPEKVDF------GVPSGKAP--GVKLNVKKIWEEYDQDPTSRPDNVIYEIS
                                                                                                                                               GDELNQKLRAYMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRES 207
                                                                                                                                                                                                                                                                                                 167;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                              5.2%; score 205; DB 15;
23.4%; Pred. No. 9.4e-08;
tive 85; Mismatches 231;
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                                                                                                700
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APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                     SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACLD AND AMINO ACID SEQUENCES
TITLE OF INVENTION: ENTEROCOCCUS FARCIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1098 LISGEKNNQITLDVT----NQAKVPLPETGGIGRLWFYLIAISTFVIAGVYLFI 1147
TELECOMMUNICATION INFORMATION:
                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085598
FILING DATE: May 14, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 451
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: pro
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                                                                                                                 643 TDKTNLEFKDGKATINLKHGE-SLTLQGLPEGYSYL---VKETDSEGYKVKVNSQEVANA 698
                                                                                                                                                                                               583 HPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELKNNKQELLSQTVK 642
                                                                                                                                                                                                                                                                            523 ELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQW 582
                                                                                                                                                                                                                                                                                                                                                                                                    491 KGAAFSLQKKEANGTYQ------PIDSQTTNEKGLASFDSLTPGKYRVVETAGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 KKTTWEIKIASDGTVTIDGKTVTTSDDTIQLTIENPFVEV--PVAVRKYAMQGTDKEINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 ISIEGNTIKSNQIY------LGKDQEIQIHYQVR--IQTENEDFHPNFWYQMNGRTT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1...728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 VNLEGS--RSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFEDY------A 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SFKRESESNLYSTSQLSLMRQALKQLIDPNLAT------KMPKQVPDDFQ--LSI 248
                                 TVSKTGITSDE-TLAFENN-KEPVVPTGVDQKINGYLALIVIAGISLGIW 746
                                                                                                                                                                                                                                                                                                                                                              LFKYTVKPRDTDPDTFLKHIKKVIEKGYREKGQAIEYSGLTETQLRAATQLAIYYFTDSA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPITFKVEAGKVYTI-IDGK------QIENPNKEIVEPYSVEAYNDFEEFSVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGDYSKLLEGATLQLTGDNVNSFQA-RVFSSNDIGERIEL-SDGTYTLTELNSPAGYSIA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTFEIQRE----HTTNAAAWKNGYIRIIKPAKDTTNTWERADIDKLSAHSGESYQEILSL
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SVLSPGAKNNQISLDITNQAKVPLPETGGIGRLGIY--LVGMIGCAFSIW
                                                                                                                                                                                                                                         DLTVHKKED-----NGQTLKGAKFRLQ-----GPEM-DLE----
                                                                                                                                                                                                                                                                                                                         GY-----DTSPGNYEFQIDKY-----GKII-YTGKNTEMTNNVWTLTHQNRLKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                            QNYAKFYYAKNKNGSSQVVYCFNADLKSPPDSE----DGGKTMTPDFTTGEVKYTHIAGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGE--KDLIGAVFKLTGDSIDTLLTDHGDGTYSLPENVKLQKEMTYTLTETKAPEGHGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQYNNQGQAFS -- YQTI ----- KELPVPGYDSQQIDAMTWKNTKQFTPLNLKITKNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FESEDKGDKYNKGYQNLLSGGLVPTKPPTPG-----DPPMPPNQPQTTSV---LIRKYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 102;
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                                                                           NLKPGTYTLTETFTPEGYQGLKEPVTIVIHEDGSIQVDGQD--HE
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                                                                                                                                                         -------GQETDTFLFE
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717
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RESULT 3 US-09-134-000-4971 ; Sequence 4971, Application US/09134000A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 4971
LENGTH: 1233
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS TITLE OF INVENTION: PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,000A CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
1151 KTGQDVPFEKIDVQGTVN--VDKIG---DYEIVYKNGKK 1184
                                                                                                                                                                                                                                                                                            991 TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI 1046
                                                                                                                                                                                                                                                                                                                                          525 DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT-----DLDFFIP-----
                                                                                                                                                                                                                                                                                                                                                                                        931 SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF
                                                                                                                                                                                                                                                                                                                                                                                                                                   482 IKKVI-----EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD----SAEL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        878 Y-----SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     788 ITGTAKEPQSNNNEGSASVSVQN---EALDILSAT------QAANPTLKNVTKT 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 YWDRGQYFDKPMTPNSPGYPTITFDENTNSYTFDFGKTNKRYII-EXKNANGWIDVPTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI----RKYAIGDYSKL---LEGATLQ 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ------NGAYSSR 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 -- VNLEGSRSYQVYCFNLKKAFP----LGSDSSVKKWYKKHDGISTKFEDYAMSPRITGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 ALVTSMVGAKTVFGLVES---STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR
                                                                                                                                         HFEIELKN-NKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETD 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV-------KGVPEDA 877
                                             SEGYKV----KVNSQEVANATVSKTGITSDETLAFENNKE 718
                                                                                              VYPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATD
                                                                                                                                                                                            DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE----KITVSGQV-DNTKAG
                                                                                                                                                                                                                                            NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTG-----DNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESESNLVSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCFNADLKSPPDSEDGGKTMTPDFTTGE---VKYTHIAGRDLFKYTVKPRDTDPDTFLKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.1%; Score lb1; DB 14; Best Local Similarity 21.1%; Pred. No. 0.00073; Matches 159; Conservative 104; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 404, Application US/09071035 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (301) 309-
TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1416 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
  802 TYTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV----
                                        368 KYYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVV 424
                                                                                                                               314 LTG-----DNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG
                                                                                                                                                                            698 YWDRGQYFDKPMTPNSPGYPTITFDENTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY 756
                                                                                                                                                                                                                                                                                                                                                    585 VIKETTPITNEIQIPIGENYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT---NSK 641
                                                                                                                                                                                                                                                                                                                                                                                                                                        532 TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK----LGT---DYTVTPTSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ------NGAYSSR 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 ALVTSMVGAKTVFGLVES---STPNAINPDSSSEYRWYGYESYVRGHPYYKOFRVAHDLR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: A. Anders Brookes REGISTRATION NUMBER: 36
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SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 -- VNLEGSRSYQVYCFNLKKAFP----LGSDSSVKKWYKKHDGISTKFEDYAMSPRITGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                   ITGTAKEPQSNNNEGSASVSVQN---EALDILSAT------QAANPTLKNVTKT 801
                                                                                                                                                                                                                   LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI----RKYAIGDYSKL---LEGATLQ 313
                                                                                                                                                                                                                                                                RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ
                                                                                                                                                                                                                                                                                                       RESESULVSTSQLSLMRQALKQLIDPULATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN 264
                                                                                                                                                                                                                                                                                                                                                                                          ELNOKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 166;
-KGVPEDA 846
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                                                                                                                                 367
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RESULT 5
US-09-071-035-402
; Sequence 402, Application US/09071035
; GENERAL INFORMATION:
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                                                                                                ; MOLECULE TYPE: protein US-09-071-035-402
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                Query Match
Best Local Similarity
  Matches
                                                                                                                                                                                                                                     TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1071
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1448 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960 TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684 EGYKV---KVNSQEVANATVSKTGITSDETLAFEN 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF
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                                                                                                                                     STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland COUNTRY: USA ZIP: 20850
                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville STATE: Maryland
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE----KITVSGQVDNXKAGV 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCFNADLKSPPDSEDGGKTMTPDFTTGE----VKYTHIAGRDLFKYTVKPRDTDPDTFLKH 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGQDVPFEKIDVQGTVN--VDKIG---DYEIVYKN 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATDK 1120
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  159;
                                                                                                                                                                                              1448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Human Genome Sciences,
9410 Key West Avenue
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA 899
                                                                                                                                                       single
                                                                                                                                                                                                                                                        309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSDOS version 6.2
4.1%; Score 161; DB 14;
21.1%; Pred. No. 0.00076;
tive 104; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD----SAEL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.50 inch, 1.4Mb
                                                                                                                                                                                                                                       402:
                                    Length 1448;
  Indels 166;
  Gaps
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                                                                                                                                                                                                                                                                                                                                                          US-08-851-567B-49
                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                              Sequence 49, Applicat
GENERAL INFORMATION:
APPLICANT: Ensign
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APPLICANT:
APPLICANT:
                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                          APPLICANT:
                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1148 TGQDVPFEKIDVQGTVN--VDKIG---DYEIVYKN 1177
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 YPIIYSDEGKEETAYVTVKPDQSKLEVKD--TTIYV--GDSWK----PE--DNFVSATDK 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045 DHSRLQVKDSTIYVGDSWKPEE--NFVSATDKTGQDVPFE-----KITVSGQVDNXKAGV 109:
                    APPLICANT
                                                                              APPLICANT:
                                                                                                   APPLICANT:
                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   987 TTDEKGQYSFDAIMTGDYTLRVTNVPQEYSVDEE--YLTGKAIKLVKGDNQLKIPLTKTI 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 IKKVI-----EKGYREKGQAIEYSGLTETQLRAATQLAIYYFTD----SAEL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    725 YWDRGQYFDKPMTPNSPGYPTITFDENTNSYTFDFGKTNKRYII-EYKNANGWIDVPTLY 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 VIKFTTPITNEIQIPIGFNYVPDSLPKDKSIPVDTIPITMSAEGLTPVDTTVTT---NSK 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 TTVSVMGSKEKPIQNLEIKVKHPNYLSLRATKEIYFYYK----LGT---DYTVTPTSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 -- VNLEGSRSYQVYCENLKKAFP----LGSDSSVKKWYKKHDGISTKFEDYAMSPRITGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 ALVTSMVGAKTVFGLVES----STPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVYT-IIDGK--QIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSTPVIGPNKAIQLVSDQYIEPISVVNP-LNAETAWGNYDQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDS 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNNKYQ-----SLIGTQWHPEDLVDIIRMEDKK-EVIPVTHNLTLRKTVTGLAGDRTKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKDKLKDYHGFGDM-NDSTLAVAKILVEYAQDSNPPQLT------DLDFFIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCFNADLKSPPDSEDGGKTMTPDFTTGE----VKYTHIAGRDLFKYTVKPRDTDPDTFLKH 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVTTKNIDNKTHRVKNPTIELTPKGTTNAQIDLNSITV-------KGVPEDA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELNOKLRAVMYNGHPQNANGIMEGLE-----PLNAIRVTQEAVWYYSDNAPISNPDESFK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKKKVTTAPITLKFSEGDAEGIVYLATATFYTHNVEDENQAIAKVSFELIDNVTHTATEF 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y-----SLEKTTNGAKVIFKDYTLTENITIEYNTVSANAGQIYTETTIDSETLNQMSA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITGTAKEPQSNNNEGSASVSVQN---EALDILSAT-----QAANPTLKNVTKT 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTG-----DNVNSFQARVFSSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSGGLVPTKPPTPGDPPMP--PNQPQTTSVLI-----RKYAIGDYSKL---LEGATLQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGSERTLQSSKNQFLVNARNDSFDSLSVRTKIPAGA--DVLFDIYDVSN--DQVDSIYPQ 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESESULVSTSQLSLMRQALKQLIDPULATKMPKQVPDDFQLSIFESEDKGDKYNKGYQN 264
                                                                                                                                                                                                                                                                                                                                       Application US/08851567B
Ciche, Todd A.
Sukhapinda, Ki
                                                                                                                                                           Rocheleau, Thomas A. Blackburn, Michael B.
                                                                                                                                                                                                Schoonover, Sue ffrench-Constant,
                                       Guo, Lining
                                                          Strickland, James
                                                                              Roberts, Jean
                                                                                                 Orr, Gregory L.
                                                                                                                                                                                                                                          Fatig, Raymond
                                                                                                                                                                                                                                                                               Ensign, Jerald
Bowen, David J
                                                                                                                    Merlo,
                                                                                                                                        Hey, Timothy D.
                                                                                                                                                                                                                                                        Petell, James
                                                                                                                      Donald J.
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  Kitisri
                                                                                                                                                                                                    Richard
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Best Local Similarity
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 1034
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
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CITY: Indianapolis
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 6 FILING DATE: 06-NOV-1995
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YWRSVDHSKFNDGKFAANAWSEWHKIDCPINPYKSTIRPVIYK---SRLYLLWLEQKEIT 1090
                                                                                                                  ENVEENANSGVISRQFFIDWDKYNKRYSTWAGVSQLVYYPENYIDPTMRIGQTKMMDALL 973
                                                                                                                                                                             SAALSTYYIRQVAKAAAAIKSRDDLYQYLLIDNQVSAAIKTTRIAEAIA-SIQLYVNRAL 913
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                                                          QSVSQSQLNADTVEDAFMSYLTSFEQVANLKVISAYHDNINNDQGLTYFIGLSETDAGEY
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                            -----RIELSDGTYTLT-----ELNSPAG--YSIAEPITFKVEAGKVYTI-IDGKQIE 379
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9330 Zionsville Road
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SYSTEM: PC-DOS/MS-DOS
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05-MAY-1997
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28-AUG-1996
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Pred. No. 0.0067;
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               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Blackburn, Michael
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rts, Jean L
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В.
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PRIOR APPLICATION DATA:

05-MAY-1997

APPLICATION NUMBER:

US 08/063,615

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Best Local Similarity
Matches 148; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/608,423
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ATTORNEY/AGENT INFORMATION:
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  1350 KIYISPKLRIIHNGYEGQKRNQCNLMNKYGKLGDKFIVYTSLGVNPNNSSNKLMFYPVYQ 1409
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                                    476 DTFLKHIKKVIEKGY----REKGQAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 28-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENGTH:
                                                                                                                                                                                                                                                                            NPNKEIVEPYSVEAYNDFE------
                                                                                                                                                                                                                                                                                                                                                                                              QSVSQSQLNADTVEDAFMSYLTSFEQVANLKVISAYHDNINNDQGLTYFIGLSETDAGEY 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVMYNGHPQNANGIMEGLEPLNAIRVTQE-AVWYYSD-----NAPISNPDESFKRESE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                     RKYA-----SSNDIGE- 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAALSTYYIRQVAKAAAAIKSRDDLYQYLLIDNQVSAAIKTTRIAEAIA-SIQLYVNRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNLVST---SQLSLMRQALKQ------LIDPNLA----TKMPKQVPDDFQL-----
                                                                             SYQQFDTNNVRRVNNRYAEDYEIPSSVSSRKDYGWGDYYLSMVYNGDIPTINYKAASSDL
                                                                                                                                                        YQGEDTLLVMFYNQQDTLDSYKNASMQGLYIF-ADMAS------KDMTPEQSNVYRDN 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SIFESEDKG------DKYNKGYQNLLSGGLVPTKPPTPGDPPMPPNQPQTTSVLI
                                                                                                                                                                                                                                   KQTGNSKDGYQTETDYRYELKLAHIRYDGTWNTPITFDVNKKISELKLEKNRAPGLYCAG
                                                                                                                                                                                                                                                                                                                                                     -----RIELSDGTYTLT-----ELNSPAG--YSIAEPITFKVEAGKYYTI-IDGKQIE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seay, Nicholas J
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28-FEB-1995
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Pred. No. 0.011;
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                                                                                                               ----DFTTGEVKYTHIAGRDLFKYTVKPRDTDP 475
                                                                                                                                                                                                                                                                            -----YAKF 411
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; ORGANISM: SFFBP
US-09-327-536-2
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SEQ ID NO 2
LENGTH: 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 191; Conservative 121; Mismatches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 022927-008
CURRENT APPLICATION NUMBER: US/09/327,536
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: US 08/714,402
PRIOR FILING DATE: 1996-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROCHA, Claudia
TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A
TITLE OF INVENTION: STREPTOCOCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                             218 -ISQDIPKIIYDSANSPLAIGKYHAENHQLIYTFTDYIAGLDKVQLSAELSLFLENKEVL 276
                                                                                                                                                         186 AVWYYSDNAPISN-PDESFK-----RESESNLVSTSQLSLMRQALKQLIDPNLATKMP 237
                                                                                                                                                                                                                                                                                                                                                             167 TEVSSGAADFYRNHAAYFKMSFELKQKDKSETINPGDTFVLQLDRRLNPKG-----
                                                                                                                                                                                                                                                                                                                                                                                                   73 ----YGYESYVRGHPYY------KQ-----FRVAHDLRVNLEGSRSYQVYCF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 KNSKRFTVTLV--GVFLMI----FALVTSMVGAKTVFGLVESSTPNAINPDSSSEYRW-- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-----QLGKGFYATFVIPPYNLSTHG 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPSFDEMNYQFNALEIDGSGLNFINNSASIDVTFTAFAEDGRKLGYESFSIPVTLKVSTD 158:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKPDDLKQYIFMTDSKGTATDVSGPVEINTAISPAKVQIIVKAGGKEQTFTADKDVSIQP 1521
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    -QNLLS---
                                                                                                                                                                                               ENTSISNEKSTIGGQEITYKGTVNYLYGNESTKESNYITNGLSNYGGSIESYNT--ETGE
                                                                                                                                                                                                                                      -----MSPRITGDELNOK--LRAVMYNGHPQNANGIMEGL-----EPLNAIRVTQE 185
                                                                                                                                                                                                                                                                                                                        NLKKAFP-----LGSDSSVKKWYKKHDGISTKFEDYA-------
                                                                                                                                                                                                                                                                                                                                                                                                                                            KTSRTWTVTVYENGYTKLVENPYNGEIISKAGSKDV----SSSLQLENPKMSVVSKYGK 166
                                          SSYGVDVTKLTLRTDITAGLGNGFQMTKRQRIDFGNNIQNKAFIIKVTGKTDQSGKPLVV 454
                                                                                                                      FVWYVYVNPNRTNIPYATMNLWGFGRARSNTSDLENDANTSSAELGEIQVYEVPEGEKLP
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GG-----LVPTKPPTPGDPPMPPNQPQTTSVLIRKYA 299
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Pred. No. 0.0045;
                                                                                 FQLSIFESEDKGDK-YNKGY--
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CURRENT APPLICATION NUMBER: US/09/200,650
CURRENT FILLING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: 60/06,815
EARLIER FILLING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 60/098,427
EARLIER FILLING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 1315
                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-200-650-5
; Sequence 5, Application US/09200650
; GENERAL INFORMATION:
; APPLICANT: Foster, Timothy J.
; APPLICANT: Eighinn, Deirdre N.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Fibrinogen-Binding Proteins from Staphylococcus
; FILE REFERENCE: 09910-0100P
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                               Query Match 3.8%; Score 149; DB 16; Best Local Similarity 20.2%; Pred. No. 0.0068; Matches 203; Conservative 93; Mismatches 336;
                                                                                                       TYPE: PRT
ORGANISM: Staphylococcus aureus
-09-200-650-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIRMEDKKEVI------PVTHNLTLRKTVTGLAGDRTKDFHFEIE----LKNNKQELLS
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NKLNTLNTQRVLSKNS--KRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VETAAPDGYEIATAITFTVNEQ--GQVTVNGKATKGDTHIVMVDAYKPTKGSGQVIDIEE 1000
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                                                             Length 1315;
                                 Indels
                                 372;
                                 Gaps
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US-09-200-650A-5
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               Sequence 5, Application US/09200650A GENERAL INFORMATION:
 APPLICANT: Foster, Timothy J.
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1077 F--EKPAGLTQTGTNTTEDDKDADGGEVDVTITDHDDFTLDNGY 1118
                                                                                                                                                                                                                                                                               964 ----VEFETPSGYTPTSVTSGNDTEKDSNGLTTTGVIKDADNMTLDSGF---YKTPKYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 TKFQYTNSESPTLVQMATLSSTGNKSVSTGNALGFTNNQSGGAGQEVYKIGNYVWEDTNK 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 D-----VNTKELT-------DVTNQYLQKITYGDNNSAVIDFGNADSAYVVWVN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 DTIPVSKNDVEFNVTIGNTTTKTTANIQYPDYVVNEKNSIGSAFTETVSHVGNKENPGYY 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 ---PQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRESESNL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 KNIGDIKDPNNGETIATAKHDTANNLITYTFTDYV-----DRFNSVQMGINYSIYMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMNDSTLAVA------KILVEYAQDSNPP-QLTDLDFFIPNNNKYQSLIGTQWHPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGISGVTVTLKDENGNVLKTVTTDADGKYKFTDLDNGNYKVEFTTPEGYTPTTVTSGSDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NAINP--DSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKA 114
                                                                   VNSQEVANATVSKTGITSDETLAFENNKEPVVPTGVDQKI-NGY
                                                                                                                                           GDYVWYDSNKDGKQDSTEKGIKDVKVTLLNEKGEVIGTTKTDENGKYCFDNLDSGKYKVI 1076
                                                                                                                                                                                                        -----LSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDSEGYKVK 689
                                                                                                                                                                                                                                                                                                                                            LVDIIRMEDKKEVIP--VTHNLTLRK-----TVTGL---AGDRTKDFHFEIELKNNKQEL 636
                                                                                                                                                                                                                                                                                                                                                                                                                       DKDEKGISGVTVTLKDENDKVLKTVTTDENGKYQFTDL-----NNGTYK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGYTPTQVGSGTDEGIDSNGTSTTGVIKDKDNDTIDSGFYKPTYNLGDYVWEDTNKNGVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKDSNGLTTTGVINGADNMTLDSGFYKTPKYNLGNYVWEDTNKDGKQ--DSTEKGISGVT
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; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-09-200-650A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 4048183799
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Green, Jamie L.
REGISTRATION NUMBER: 32467
REFERENCE/DOCKET NUMBER: 09910-0100P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 4048183700
TELEPAX: 4048183799
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TITLE OF INVENTION: Fibrinogen-Binding Pr
TITLE OF INVENTION: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: USA
481 D-----VNTKELT-----DVTNQYLQKITYGDNNSAVIDFGNADSAYVVMVN 522
                                        263 QNLLSGGLVPTKPPTPGDPPMPPNQPQTTSVLIRKYAIGDYSK----------
                                                                                         425 KQTIYUNDSENSLTNAKLKVQAYHSSYPNNIGQINKDVTD---IKIYQ-VPKGYTLNKGY 480
                                                                                                                                                                                          365 DTIPVSKNDVEFNVTIGNTTTKTTANIQYPDYVVNEKNSIGSAFTETVSHVGNKENPGYY 424
                                                                                                                                                                                                                                          164 --- PQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRESESNL------
                                                                                                                                                                                                                                                                                             312 KNIGDIKDPNNGETIATAKHDTANNLITYTFTDYV------DRFNSVQMGINYSIYMDA 364
                                                                                                                                                                                                                                                                                                                                           115 FPLGS----DSSVKKWYKKHDG----ISTKFEDYAMSPRITGDELNQKLRAVMYNGH--- 163
                                                                                                                                                                                                                                                                                                                                                                                            263 DKNNKIVPAQDYLSLKSQITVDDKVKSGDYF-----TIKYSDTVQVYGLNPEDI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 NSNNENNADIILPKSTAPKRLNTR-----MRIAAVQPSSTEAKNVNDLITSNTTLTVVDA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ---NAINP--DSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/200,650A
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                                                                                                                                         -----VSTSQLSLMRQALK----QLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGY 262
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uence 458, Application US/09071035 uence 458, Application US/09071035 MERAL IMFORMATION: APPLICANT: Gil H. Choi ITTLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polype CORRESPONDENCE S: 496 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION NUMBER: US/09/071,035 FILING DATE: CLASSIFICATION UMBER: US/09/071,035 APPLICATION UMBER: US/09/071,035 APPLICATION INFORMATION: APPLICATION INFORMATION: APPLICATION INFORMATION: APPLICATION INFORMATION: APPLICATION INFORMATION: APPLICATION INFORMATION:	RESULT 11 US-09-071-03 ; Sequence 4 ; GENERAL 1 ; APPLICE TITLE (NUMBER CORRESI ADDRE STAFF COMPUTI STAFF COMPUTI MEDIC MED	
VNSQEVANÁTVSKTGITSDETLAFENNKEPVVPTGVDQKI-NGY 732 :	Qy 690 Db 1077	
LSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGYSYLVKETDSEGYKVK 689 ::	Qy 637 Db 1017	
LVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELKNNKQEL 636 :	Qy 587 Db 964	
DMNDSTLAVAKILVEYAQDSNPP-QLTDLDFFIPNNNKYQSLIGTQWHPED 586 : :	Qу 537 рь 920	
SGLTETQLRAATQLAI-YYFTDSAELDKDKLKDYHGFG 536	Qy 500 рь 860	
MTPDFTTGEVKYTHIAGRD-LFKYTVKPRDTDPDTFLKHIKKVIEKGYREKGQAIEY 499 :	Qy 444 Db 821	
EEFS-VLTTQNYAKFYYAKNKNGSSQVVYCFNADLKSPPDSEDGGKT 443 :	Qу 398 Db 763	
PITFKVEAGKVYTIIDGKQIENPNKEIVEPYSVEAYNDF 397	Qy 359 Db 703	
IAE	Qy 356 Db 643	
- U	Qy 320 рь 583	
TKFQYTNSESPTLYQMATLSSTGNKSYSTGNALGFTNNQSGGAGQEVYKIGNYYWEDTNK 582	Qy 306 Db 523	

PB369P2

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1406
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1465 KPAVVVASDNFVSYKGAFQIVKTNSADQPLAGAV----FELY-DHNKQSLGITATSGKDG 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1303 PLAGAEFSVLDTTGQAVREHLYSDANGKVTVTDLAPGKYQF----VETKAP------ 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2032 amino acids
631 NNKQELLSQTV--KTDKTNLEFKDGKATI-NLKHGESLTLQGLPEGY------SYLV 678
                                                                                                                                                                                                                                                                                                                                                                                                                449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 LVSTSQLSLM----RQALKQ--LIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQNL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 VKKW----YKKHDGISTKF---EDYAMSPRITGDELNQKLRAVMYNGHPQNANGIME--G 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECUTATE: (301) 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LSKNSKRFTVTLVGVFLMIFALVTSMV------GAKTVFG-----LVESSTPNAI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAPTGYLLDTTLHP---FDVTAQLGKEQPIALGDLINYQGTA----
                                                                                                                                                                        QTLAGAVFAIYNADEQNQPQGSPITFLNRAGEKVSEITTDKTGEIYAKGLNEGHYVLVET 1745
                                                                                                                                                                                                                    STLAVAKILVEYAQDSNPPQLTDLDFFIPNNNKYQS--------
                                                                                                                                                                                                                                                                 DLGAGSYELDELDATDGYIVNKQPIYFVVKKNSNDKQPLDELEFVNYQAEVMGRKVNEQG
                                                                                                                                                                                                                                                                                                                                                               QLG--AFANFKGRAVFKKIDANANPLPGTIFKLYR--IENGEKIFEREVTAEKDGSLAME 1629
                                                                                                                                                                                                                                                                                                                                                                                                           TTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLKHIKKVIEKGYR-----EKGQAI--- 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIIFRDLAPGTYYYKEIKAPKLPDGADYIIYPELVKVEIRGDFKGDPEI-----F 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FYYAKNK-----NGSSQVVYC-----FNADLKSPPDSEDGGKTMTPDF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -AGYLLNTEPSAFTIAASDRGKPATVIATANFVNYQGTAKLIKKDVNG---HLLSGATFK 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKPGLYQFTEIEAPTGYLLDTTPKRFIVTQNTSGQIRDVHVKMLNYQGSAELIKKDQAGN 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEP-LNAIRVTQEAVWYYSDNAP-------ISNPDESFKRESESN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKKLVNARFKLEHAVTTPFTHWEEVPLAPDRT------NANGQLEVDS 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EGYTVSDELAKGRVITIDEETSAEGAQP-TIIKNDVNKVFLEKMDEK 1200
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                                                                                                                                                                                                                                                                                                                ----EYSGLTETQLRAATQLAIYYF----TDSAELDKDKLKDYHG--FG---DMND 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSGGLVPTKPPTPGDPPMPPNQPQT-----TSVLIRKYAIGDYSKLLEGATLQ 313
                                                                                                                         -----LIGTQWHPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELK 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAK--
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GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     Matches 178;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION UNMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
  1243
                                                                                                                                                                                                                                                    1098 LKKTAMDETTILAGAHFQIWDQAKTQVLREGTVDATGVITFGGLPQGQYILVETKAP--- 1154
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LENGTH: 2032 amino aci
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                                         174 LEP-LNAIRVTQEAVWYYSDNAP-----
                                                                                                                          123 VKKW----YKKHDGISTKF---EDYAMSPRITGDELNQKLRAVMYNGHPQNANGIME--G 173
                                                                                                                                                                                                                                                                                           19 LSKNSKRFTVTLVGVFLMIFALVTSMV------GAKTVFG-----LVESSTPNAI 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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LKPGLYQFTEIEAPTGYLLDTTPKRFIVTQNTSGQIRDVHVKMLNYQGSAELIKKDQAGN 1302
                                                                                  GKKLVNARFKLEHAVTTPFTHWEEVPLAPDRT----
                                                                                                                                                                   ------EGYTVSDELAKGRVITIDEETSAEGAQP-TIIKNDVNKVFLEKMDEK 1200
                                                                                                                                                                                                        NPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2032 amino acids
                                                                                                                                                                                                                                                                                                                                     Conservative 117; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B: Diskette, 3.50 inch, 1.4Mb storage HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 149; DB 14; Length 2032; 19.0%; Pred. No. 0.014;
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                                         -----ISNPDESFKRESESN 210
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                                                                                  -----NANGQLEVDS 1242
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RESULT 13
US-09-071-035-466
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                                                                                                                                                                                                                                                                                                                                         Sequence 466, Application US/09071035
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus
NUMBER OF SEQUENCES: 496
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1909 TVARSLRSDNQGLVQVNHLQPGKYTFVETKAPDGY 1943
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                                                                             MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VEI
                                                                                                                                                                                 COUNTRY: UZIP: 20850
                                                                                                                                                                                                                             CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNKQELLSQTV--KTDKTNLEFKDGKATI-NLKHGESLTLQGLPEGY-----SYLV 678
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                                                                                                                                                                                                                                                                     9410 Key West Avenue
                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                               Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYYAKNK-----NGSSQVVYC-----FNADLKSPPDSEDGGKTMTPDF
                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis
                                                                                                                                  3.50 inch, 1.4Mb storage
                                                                                           version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VKVNSQEVANA------
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2032 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1303 PLAGAEFSVLDTTGQAVREHLVSDANGKVTVTDLAPGKYQF----VETKAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: sir
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-----LIGTQWHPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTGLAGDRTKDFHFEIELK 630
                                                                                  QTLAGAVFAIYNADEQNQPQGSPITFLNRAGEKVSEITTDKTGEIYAKGLNEGHYVLVET
                                                                                                                                                             STLAVAKILVEYAQDSNPPQLTDLDFFIPNNKYQS:
                                                                                                                                                                                                                                            DLGAGSYELDELDATDGYIVNKQPIYFVVKKNSNDKQPLDELEFVNYQAEVMGRKVNEQG
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
FILE REFERENCE: GTC-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.8%; Score 149; DB 15; Length 2054; Best Local Similarity 19.0%; Pred. No. 0.014; Matches 178; Conservative 117; Mismatches 330; Indels 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 6612
LENGTH: 2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/134,000A CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                        314 LTGDNVNSFQARVFSSNDIGERI--ELSDGTYTLTELNSPAGYSI-AEPITFKV---EAG 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKKLVNARFKLEHAVTTPFTHWEEVPLAPDRT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKKW----YKKHDGISTKF---EDYAMSPRITGDELNQKLRAVMYNGHPQNANGIME--G 173
                                                                                                                                                                             VLDAKGETIQTGL-TTNNQGEIVAEHLAPGKYRFVETKAPTGYLLNTTPVPFEIAEKNAG
                                                                                                                                                                                                                                                                                                                    LSGGLVPTKPPTPGDPPMPPNQPQT-----TSVLIRKYAIGDYSKLLEGATLQ 313
                                                                                                                                                                                                                                                                                                                                                                                                               LVSTSQLSLM----RQALKQ--LIDPNLATKMPKQVPDDFQLSIFESEDKGDKYNKGYQNL
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                                                                                      KPAVVVASDNFVSYKGAFQIVKTNSADQPLAGAV----FELY-DHNKQSLGITATSGKDG 1541
                                                                                                                                                                                                                                                                           -AGYLLNTEPSAFTIAASDRGKPATVIATANFVNYQGTAKLIKKDVNG---HLLSGATFK 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEP-LNAIRVTQEAVWYYSDNAP------ISNPDESFKRESESN 210
                                           --FYYAKNK-----NGSSQVVYC----FNADLKSPPDSEDGGKTMTPDF
                                                                                                                                    --VYTIIDGKQIENPNKEIVEPYSVEAYNDFEEFSVLTTQNYAK--
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4438
LENGTH: 1349
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4438, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, RW
APPLICANT: Oblsen, KL
APPLICANT: 2yskind, JW
APPLICANT: Trawick, JD
APPLICANT: Trawick, JD
APPLICANT: Trawick, JD
APPLICANT: Trawick, JD
TITLE OF INVENTION: decruginosa, Klebsiella pneumoniae, Salmonella typhimurium,
TITLE OF INVENTION: faecalis
FILE REFERENCE: ELITRA.017PR5
CURRENT APPLICATION NUMBER: US/60/269,308
CURRENT FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1931 TVARSLRSDNQGLVQVNHLQPGKYTFVETKAPDGY 1965
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  365
                                                                                         312 KNIGDIKDPNNGETIATAKHDTANNLITYTFTDYV-----DRFNSVQMGINYSIYMDA 364
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                                            164 --- PQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNPDESFKRESESNL-----
                                                                                                                                                                                                                                                                         208 NSNNENNADIILPKSTAPKRLNTR----MRIAAVQPSSTEAKNVNDLITSNTTLTVVDA 262
                                                                                                                                                                                                                          60 ---NAINP--DSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKA 114
                                                                                                                                                                                                                                                                                                                   8
DTIPVSKNDVEFNVTIGNTTTKTTANIQYPDYVVNEKNSIGSAFTETVSHVGNKENPGYY 424
                                                                                                                                   FPLGS----DSSVKKWYKKHDG----ISTKFEDYAMSPRITGDELNQKLRAVMYNGH--- 163
                                                                                                                                                                                DKNNKIVPAQDYLSLKSQITVDDKVKSGDYF-----TIKYSDTVQVYGLNPEDI 311
                                                                                                                                                                                                                                                                                                                 NKLNTLNTORVLSKNS--KRETVTLVGVFLMIFALVTSMVGAKTVFGLVESSTP-----
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                                                                                                                                                                                                                                                                                                                                                                203;
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                3.7%; Score 147; DB 20.2%; Pred. No. 0.01;
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                                                                                                                                                                                                                                                                                                                                                                91; Mismatches 338;
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Search completed: June 7, 2001, 00:20:50 Job time: 193 sec